SEQUENCE LISTING

<110> VAN HIJUM, SACHA ADRIANUS FOKKE TACO
VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
DIJKHUIZEN, LUBBERT
RAHAOUI, HAKIM

<120> NOVEL FRUCTOSYLTRANSFERASES

<130> 2001-1043-2

<140>
<141>

<150> 09/995,587
<151> 2001-11-29

<150> 09/604,958
<151> 2000-06-28

<150> EPO 00201872.9
<151> 2000-05-25

<160> 40

<170> PatentIn Ver. 2.1

<210> 1
<211> 789
<212> PRT
<213> Lactobacillus reuteri

<400> 1

```
Met Tyr Lys Ser Gly Lys Asn Trp Ala Val Val Thr Leu Ser Thr Ala
  1               5                  10                  15

Ala Leu Val Phe Gly Ala Thr Thr Val Asn Ala Ser Ala Asp Thr Asn
             20                  25                  30

Ile Glu Asn Asn Asp Ser Ser Thr Val Gln Val Thr Thr Gly Asp Asn
         35                  40                  45

Asp Ile Ala Val Lys Ser Val Thr Leu Gly Ser Gly Gln Val Ser Ala
     50                  55                  60

Ala Ser Asp Thr Thr Ile Arg Thr Ser Ala Asn Ala Asn Ser Ala Ser
 65                  70                  75                  80

Ser Ala Ala Asn Thr Gln Asn Ser Asn Ser Gln Val Ala Ser Ser Ala
                 85                  90                  95

Ala Ile Thr Ser Ser Thr Ser Ser Ala Ala Ser Leu Asn Asn Thr Asp
            100                 105                 110

Ser Lys Ala Ala Gln Glu Asn Thr Asn Thr Ala Lys Asn Asp Asp Thr
        115                 120                 125

Gln Lys Ala Ala Pro Ala Asn Glu Ser Ser Glu Ala Lys Asn Glu Pro
    130                 135                 140

Ala Val Asn Val Asn Asp Ser Ser Ala Ala Lys Asn Asp Asp Gln Gln
```

```
145                 150                 155                 160

Ser Ser Lys Lys Asn Thr Thr Ala Lys Leu Asn Lys Asp Ala Glu Asn
                165                 170                 175

Val Val Lys Lys Ala Gly Ile Asp Pro Asn Ser Leu Thr Asp Asp Gln
            180                 185                 190

Ile Lys Ala Leu Asn Lys Met Asn Phe Ser Lys Ala Ala Lys Ser Gly
        195                 200                 205

Thr Gln Met Thr Tyr Asn Asp Phe Gln Lys Ile Ala Asp Thr Leu Ile
    210                 215                 220

Lys Gln Asp Gly Arg Tyr Thr Val Pro Phe Phe Lys Ala Ser Glu Ile
225                 230                 235                 240

Lys Asn Met Pro Ala Ala Thr Thr Lys Asp Ala Gln Thr Asn Thr Ile
                245                 250                 255

Glu Pro Leu Asp Val Trp Asp Ser Trp Pro Val Gln Asp Val Arg Thr
            260                 265                 270

Gly Gln Val Ala Asn Trp Asn Gly Tyr Gln Leu Val Ile Ala Met Met
        275                 280                 285

Gly Ile Pro Asn Gln Asn Asp Asn His Ile Tyr Leu Leu Tyr Asn Lys
    290                 295                 300

Tyr Gly Asp Asn Glu Leu Ser His Trp Lys Asn Val Gly Pro Ile Phe
305                 310                 315                 320

Gly Tyr Asn Ser Thr Ala Val Ser Gln Glu Trp Ser Gly Ser Ala Val
                325                 330                 335

Leu Asn Ser Asp Asn Ser Ile Gln Leu Phe Tyr Thr Arg Val Asp Thr
            340                 345                 350

Ser Asp Asn Asn Thr Asn His Gln Lys Ile Ala Ser Ala Thr Leu Tyr
        355                 360                 365

Leu Thr Asp Asn Asn Gly Asn Val Ser Leu Ala Gln Val Arg Asn Asp
    370                 375                 380

Tyr Ile Val Phe Glu Gly Asp Gly Tyr Tyr Tyr Gln Thr Tyr Asp Gln
385                 390                 395                 400

Trp Lys Ala Thr Asn Lys Gly Ala Asp Asn Ile Ala Met Arg Asp Ala
                405                 410                 415

His Val Ile Glu Asp Gly Asn Gly Asp Arg Tyr Leu Val Phe Glu Ala
            420                 425                 430

Ser Thr Gly Leu Glu Asn Tyr Gln Gly Glu Asp Gln Ile Tyr Asn Trp
        435                 440                 445

Leu Asn Tyr Gly Gly Asp Asp Ala Phe Asn Ile Lys Ser Leu Phe Arg
    450                 455                 460

Ile Leu Ser Asn Asp Asp Ile Lys Ser Arg Ala Thr Trp Ala Asn Ala
465                 470                 475                 480
```

Ala Ile Gly Ile Leu Lys Leu Asn Lys Asp Glu Lys Asn Pro Lys Val
485 490 495

Ala Glu Leu Tyr Ser Pro Leu Ile Ser Ala Pro Met Val Ser Asp Glu
500 505 510

Ile Glu Arg Pro Asn Val Val Lys Leu Gly Asn Lys Tyr Tyr Leu Phe
515 520 525

Ala Ala Thr Arg Leu Asn Arg Gly Ser Asn Asp Asp Ala Trp Met Asn
530 535 540

Ala Asn Tyr Ala Val Gly Asp Asn Val Ala Met Val Gly Tyr Val Ala
545 550 555 560

Asp Ser Leu Thr Gly Ser Tyr Lys Pro Leu Asn Asp Ser Gly Val Val
565 570 575

Leu Thr Ala Ser Val Pro Ala Asn Trp Arg Thr Ala Thr Tyr Ser Tyr
580 585 590

Tyr Ala Val Pro Val Ala Gly Lys Asp Asp Gln Val Leu Val Thr Ser
595 600 605

Tyr Met Thr Asn Arg Asn Gly Val Ala Gly Lys Gly Met Asp Ser Thr
610 615 620

Trp Ala Pro Ser Phe Leu Leu Gln Ile Asn Pro Asp Asn Thr Thr Thr
625 630 635 640

Val Leu Ala Lys Met Thr Asn Gln Gly Asp Trp Ile Trp Asp Asp Ser
645 650 655

Ser Glu Asn Leu Asp Met Ile Gly Asp Leu Asp Ser Ala Ala Leu Pro
660 665 670

Gly Glu Arg Asp Lys Pro Val Asp Trp Asp Leu Ile Gly Tyr Gly Leu
675 680 685

Lys Pro His Asp Pro Ala Thr Pro Asn Asp Pro Glu Thr Pro Thr Thr
690 695 700

Pro Glu Thr Pro Glu Thr Pro Asn Thr Pro Lys Thr Pro Lys Thr Pro
705 710 715 720

Glu Asn Pro Gly Thr Pro Gln Thr Pro Asn Thr Pro Asn Thr Pro Glu
725 730 735

Ile Pro Leu Thr Pro Glu Thr Pro Lys Gln Pro Glu Thr Gln Thr Asn
740 745 750

Asn Arg Leu Pro Gln Thr Gly Asn Asn Ala Asn Lys Ala Met Ile Gly
755 760 765

Leu Gly Met Gly Thr Leu Leu Ser Met Phe Gly Leu Ala Glu Ile Asn
770 775 780

Lys Arg Arg Phe Asn
785

<210> 2
<211> 2367
<212> DNA
<213> Lactobacillus reuteri

<400> 2
atgtataaaa gcggtaaaaa ttgggcagtc gttacactct cgactgctgc gctggtattt 60
ggtgcaacaa ctgtaaatgc atccgcggac acaaatattg aaaacaatga ttcttctact 120
gtacaagtta caacaggtga taatgatatt gctgttaaaa gtgtgacact tggtagtggt 180
caagttagtg cagctagtga tacgactatt agaacttctg ctaatgcaaa tagtgcttct 240
tctgccgcta atacacaaaa ttctaacagt caagtagcaa gttctgctgc aataacatca 300
tctacaagtt ccgcagcttc attaaataac acagatagta aagcggctca agaaaatact 360
aatacagcca aaaatgatga cacgcaaaaa gctgcaccag ctaacgaatc ttctgaagct 420
aaaaatgaac cagctgtaaa cgttaatgat tcttcagctg caaaaaatga tgatcaacaa 480
tccagtaaaa agaatactac cgctaagtta aacaaggatg ctgaaaacgt tgtaaaaaag 540
gcgggaattg atcctaacag tttaactgat gaccagatta aagcattaaa taagatgaac 600
ttctcgaaag ctgcaaagtc tggtacacaa atgacttata atgatttcca aaagattgct 660
gatacgttaa tcaaacaaga tggtcggtac acagttccat tctttaaagc aagtgaaatc 720
aaaaatatgc ctgccgctac aactaaagat gcacaaacta atactattga acctttagat 780
gtatgggatt catggccagt tcaagatgtt cggacaggac aagttgctaa ttggaatggc 840
tatcaacttg tcatcgcaat gatgggaatt ccaaaccaaa atgataatca tatctatctc 900
ttatataata agtatggtga taatgaatta agtcattgga agaatgtagg tccaattttt 960
ggctataatt ctaccgcggt ttcacaagaa tggtcaggat cagctgtttt gaacagtgat 1020
aactctatcc aattatttta tacaagggta gacacgtctg ataacaatac caatcatcaa 1080
aaaattgcta gcgctactct ttatttaact gataataatg gaaatgtatc actcgctcag 1140
gtacgaaatg actatattgt atttgaaggt gatggctatt actaccaaac ttatgatcaa 1200
tggaaagcta ctaacaaagg tgccgataat attgcaatgc gtgatgctca tgtaattgaa 1260
gatggtaatg gtgatcggta ccttgttttt gaagcaagta ctggtttgga aaattatcaa 1320
ggcgaggacc aaatttataa ctggttaaat tatggcggag atgacgcatt taatatcaag 1380
agcttattta gaattctttc caatgatgat attaagagtc gggcaacttg ggctaatgca 1440
gctatcggta tcctcaaact aaataaggac gaaaagaatc ctaaggtggc agagttatac 1500
tcaccattaa tttctgcacc aatggtaagc gatgaaattg agcgaccaaa tgtagttaaa 1560
ttaggtaata aatattactt atttgccgct acccgtttaa atcgaggaag taatgatgat 1620
gcttggatga atgctaatta tgccgttggt gataatgttg caatggtcgg atatgttgct 1680
gatagtctaa ctggatctta taagccatta aatgattctg gagtagtctt gactgcttct 1740
gttcctgcaa actggcggac agcaacttat tcatattatg ctgtccccgt tgccggaaaa 1800
gatgaccaag tattagttac ttcatatatg actaatagaa atggagtagc gggtaaagga 1860
atggattcaa cttgggcacc gagtttctta ctacaaatta acccggataa cacaactact 1920
gttttagcta aaatgactaa tcaaggggat tggatttggg atgattcaag cgaaaatctt 1980
gatatgattg gtgatttaga ctccgctgct ttacctggcg aacgtgataa acctgttgat 2040
tgggacttaa ttggttatgg attaaaaccg catgatcctg ctacaccaaa tgatcctgaa 2100
acgccaacta caccagaaac ccctgagaca cctaatactc ccaaaacacc aaagactcct 2160
gaaaatcctg ggacacctca aactcctaat acacctaata ctccggaaat tcctttaact 2220
ccagaaacgc ctaagcaacc tgaaacccaa actaataatc gtttgccaca aactggaaat 2280
aatgccaata aagccatgat tggcctaggt atgggaacat tgcttagtat gtttggtctt 2340
gcagaaatta acaaacgtcg atttaac 2367

<210> 3
<211> 2394
<212> DNA
<213> Lactobacillus reuteri

<400> 3
atgctagaac gcaaggaaca taaaaaaatg tataaaagcg gtaaaaattg ggcagtcgtt 60
acactctcga ctgctgcgct ggtatttggt gcaacaactg taaatgcatc cgcggacaca 120
aatattgaaa acaatgattc ttctactgta caagttacaa caggtgataa tgatattgct 180
gttaaaagtg tgacacttgg tagtggtcaa gttagtgcag ctagtgatac gactattaga 240
acttctgcta atgcaaatag tgcttcttct gccgctaata cacaaaattc taacagtcaa 300
gtagcaagtt ctgctgcaat aacatcatct acaagttccg cagcttcatt aaataacaca 360

```
gatagtaaag cggctcaaga aaatactaat acagccaaaa atgatgacac gcaaaaagct 420
gcaccagcta acgaatcttc tgaagctaaa aatgaaccag ctgtaaacgt taatgattct 480
tcagctgcaa aaaatgatga tcaacaatcc agtaaaaaga atactaccgc taagttaaac 540
aaggatgctg aaaacgttgt aaaaaaggcg ggaattgatc ctaacagttt aactgatgac 600
cagattaaag cattaaataa gatgaacttc tcgaaagctg caaagtctgg tacacaaatg 660
acttataatg atttccaaaa gattgctgat acgttaatca aacaagatgg tcggtacaca 720
gttccattct ttaaagcaag tgaaatcaaa aatatgcctg ccgctacaac taaagatgca 780
caaactaata ctattgaacc tttagatgta tgggattcat ggccagttca agatgttcgg 840
acaggacaag ttgctaattg gaatggctat caacttgtca tcgcaatgat gggaattcca 900
aaccaaaatg ataatcatat ctatctctta tataataagt atggtgataa tgaattaagt 960
cattggaaga atgtaggtcc aatttttggc tataattcta ccgcggtttc acaagaatgg 1020
tcaggatcag ctgttttgaa cagtgataac tctatccaat tattttatac aagggtagac 1080
acgtctgata acaataccaa tcatcaaaaa attgctagcg ctactcttta tttaactgat 1140
aataatggaa atgtatcact cgctcaggta cgaaatgact atattgtatt tgaaggtgat 1200
ggctattact accaaactta tgatcaatgg aaagctacta acaaaggtgc cgataatatt 1260
gcaatgcgtg atgctcatgt aattgaagat ggtaatggtg atcggtacct tgtttttgaa 1320
gcaagtactg gtttggaaaa ttatcaaggc gaggaccaaa tttataactg gttaaattat 1380
ggcggagatg acgcatttaa tatcaagagc ttatttagaa ttctttccaa tgatgatatt 1440
aagagtcggg caacttgggc taatgcagct atcggtatcc tcaaactaaa taaggacgaa 1500
aagaatccta aggtggcaga gttatactca ccattaattt ctgcaccaat ggtaagcgat 1560
gaaattgagc gaccaaatgt agttaaatta ggtaataaat attacttatt tgccgctacc 1620
cgtttaaatc gaggaagtaa tgatgatgct tggatgaatg ctaattatgc cgttggtgat 1680
aatgttgcaa tggtcggata tgttgctgat agtctaactg gatcttataa gccattaaat 1740
gattctggag tagtcttgac tgcttctgtt cctgcaaact ggcggacagc aacttattca 1800
tattatgctg tccccgttgc cggaaaagat gaccaagtat tagttacttc atatatgact 1860
aatagaaatg gagtagcggg taaaggaatg gattcaactt gggcaccgag tttcttacta 1920
caaattaacc cggataacac aactactgtt ttagctaaaa tgactaatca aggggattgg 1980
atttgggatg attcaagcga aaatcttgat atgattggtg atttagactc cgctgcttta 2040
cctggcgaac gtgataaacc tgttgattgg gacttaattg gttatggatt aaaaccgcat 2100
gatcctgcta caccaaatga tcctgaaacg ccaactacac cagaaacccc tgagacacct 2160
aatactccca aaacaccaaa gactcctgaa aatcctggga cacctcaaac tcctaataca 2220
cctaatactc cggaaattcc tttaactcca gaaacgccta agcaacctga aacccaaact 2280
aataatcgtt tgccacaaac tggaaataat gccaataaag ccatgattgg cctaggtatg 2340
ggaacattgc ttagtatgtt tggtcttgca gaaattaaca aacgtcgatt taac       2394
```

<210> 4
<211> 2592
<212> DNA
<213> Lactobacillus reuteri

<220>
<221> CDS
<222> (1)..(51)

<220>
<221> CDS
<222> (68)..(2434)

<400> 4

```
tac aat ggg gtg gcg gag gtg aag aaa cgg ggt tac ttc tat gct aga   48
Tyr Asn Gly Val Ala Glu Val Lys Lys Arg Gly Tyr Phe Tyr Ala Arg
  1               5                  10                  15

acg caaggaacat aaaaaa atg tat aaa agc ggt aaa aat tgg gca gtc gtt 100
Thr                   Met Tyr Lys Ser Gly Lys Asn Trp Ala Val Val
                           20                  25

aca ctc tcg act gct gcg ctg gta ttt ggt gca aca act gta aat gca   148
Thr Leu Ser Thr Ala Ala Leu Val Phe Gly Ala Thr Thr Val Asn Ala
     30                  35                  40
```

```
tcc gcg gac aca aat att gaa aac aat gat tct tct act gta caa gtt   196
Ser Ala Asp Thr Asn Ile Glu Asn Asn Asp Ser Ser Thr Val Gln Val
 45                  50                  55                  60

aca aca ggt gat aat gat att gct gtt aaa agt gtg aca ctt ggt agt   244
Thr Thr Gly Asp Asn Asp Ile Ala Val Lys Ser Val Thr Leu Gly Ser
                 65                  70                  75

ggt caa gtt agt gca gct agt gat acg act att aga act tct gct aat   292
Gly Gln Val Ser Ala Ala Ser Asp Thr Thr Ile Arg Thr Ser Ala Asn
             80                  85                  90

gca aat agt gct tct tct gcc gct aat aca caa aat tct aac agt caa   340
Ala Asn Ser Ala Ser Ser Ala Ala Asn Thr Gln Asn Ser Asn Ser Gln
         95                 100                 105

gta gca agt tct gct gca ata aca tca tct aca agt tcc gca gct tca   388
Val Ala Ser Ser Ala Ala Ile Thr Ser Ser Thr Ser Ser Ala Ala Ser
    110                 115                 120

tta aat aac aca gat agt aaa gcg gct caa gaa aat act aat aca gcc   436
Leu Asn Asn Thr Asp Ser Lys Ala Ala Gln Glu Asn Thr Asn Thr Ala
125                 130                 135                 140

aaa aat gat gac acg caa aaa gct gca cca gct aac gaa tct tct gaa   484
Lys Asn Asp Asp Thr Gln Lys Ala Ala Pro Ala Asn Glu Ser Ser Glu
                145                 150                 155

gct aaa aat gaa cca gct gta aac gtt aat gat tct tca gct gca aaa   532
Ala Lys Asn Glu Pro Ala Val Asn Val Asn Asp Ser Ser Ala Ala Lys
            160                 165                 170

aat gat gat caa caa tcc agt aaa aag aat act acc gct aag tta aac   580
Asn Asp Asp Gln Gln Ser Ser Lys Lys Asn Thr Thr Ala Lys Leu Asn
        175                 180                 185

aag gat gct gaa aac gtt gta aaa aag gcg gga att gat cct aac agt   628
Lys Asp Ala Glu Asn Val Val Lys Lys Ala Gly Ile Asp Pro Asn Ser
    190                 195                 200

tta act gat gac cag att aaa gca tta aat aag atg aac ttc tcg aaa   676
Leu Thr Asp Asp Gln Ile Lys Ala Leu Asn Lys Met Asn Phe Ser Lys
205                 210                 215                 220

gct gca aag tct ggt aca caa atg act tat aat gat ttc caa aag att   724
Ala Ala Lys Ser Gly Thr Gln Met Thr Tyr Asn Asp Phe Gln Lys Ile
                225                 230                 235

gct gat acg tta atc aaa caa gat ggt cgg tac aca gtt cca ttc ttt   772
Ala Asp Thr Leu Ile Lys Gln Asp Gly Arg Tyr Thr Val Pro Phe Phe
            240                 245                 250

aaa gca agt gaa atc aaa aat atg cct gcc gct aca act aaa gat gca   820
Lys Ala Ser Glu Ile Lys Asn Met Pro Ala Ala Thr Thr Lys Asp Ala
        255                 260                 265

caa act aat act att gaa cct tta gat gta tgg gat tca tgg cca gtt   868
Gln Thr Asn Thr Ile Glu Pro Leu Asp Val Trp Asp Ser Trp Pro Val
    270                 275                 280
```

```
caa gat gtt cgg aca gga caa gtt gct aat tgg aat ggc tat caa ctt   916
Gln Asp Val Arg Thr Gly Gln Val Ala Asn Trp Asn Gly Tyr Gln Leu
285                 290                 295                 300

gtc atc gca atg atg gga att cca aac caa aat gat aat cat atc tat   964
Val Ile Ala Met Met Gly Ile Pro Asn Gln Asn Asp Asn His Ile Tyr
                305                 310                 315

ctc tta tat aat aag tat ggt gat aat gaa tta agt cat tgg aag aat   1012
Leu Leu Tyr Asn Lys Tyr Gly Asp Asn Glu Leu Ser His Trp Lys Asn
            320                 325                 330

gta ggt cca att ttt ggc tat aat tct acc gcg gtt tca caa gaa tgg   1060
Val Gly Pro Ile Phe Gly Tyr Asn Ser Thr Ala Val Ser Gln Glu Trp
        335                 340                 345

tca gga tca gct gtt ttg aac agt gat aac tct atc caa tta ttt tat   1108
Ser Gly Ser Ala Val Leu Asn Ser Asp Asn Ser Ile Gln Leu Phe Tyr
    350                 355                 360

aca agg gta gac acg tct gat aac aat acc aat cat caa aaa att gct   1156
Thr Arg Val Asp Thr Ser Asp Asn Asn Thr Asn His Gln Lys Ile Ala
365                 370                 375                 380

agc gct act ctt tat tta act gat aat aat gga aat gta tca ctc gct   1204
Ser Ala Thr Leu Tyr Leu Thr Asp Asn Asn Gly Asn Val Ser Leu Ala
                385                 390                 395

cag gta cga aat gac tat att gta ttt gaa ggt gat ggc tat tac tac   1252
Gln Val Arg Asn Asp Tyr Ile Val Phe Glu Gly Asp Gly Tyr Tyr Tyr
            400                 405                 410

caa act tat gat caa tgg aaa gct act aac aaa ggt gcc gat aat att   1300
Gln Thr Tyr Asp Gln Trp Lys Ala Thr Asn Lys Gly Ala Asp Asn Ile
        415                 420                 425

gca atg cgt gat gct cat gta att gaa gat ggt aat ggt gat cgg tac   1348
Ala Met Arg Asp Ala His Val Ile Glu Asp Gly Asn Gly Asp Arg Tyr
    430                 435                 440

ctt gtt ttt gaa gca agt act ggt ttg gaa aat tat caa ggc gag gac   1396
Leu Val Phe Glu Ala Ser Thr Gly Leu Glu Asn Tyr Gln Gly Glu Asp
445                 450                 455                 460

caa att tat aac tgg tta aat tat ggc gga gat gac gca ttt aat atc   1444
Gln Ile Tyr Asn Trp Leu Asn Tyr Gly Gly Asp Asp Ala Phe Asn Ile
                465                 470                 475

aag agc tta ttt aga att ctt tcc aat gat gat att aag agt cgg gca   1492
Lys Ser Leu Phe Arg Ile Leu Ser Asn Asp Asp Ile Lys Ser Arg Ala
            480                 485                 490

act tgg gct aat gca gct atc ggt atc ctc aaa cta aat aag gac gaa   1540
Thr Trp Ala Asn Ala Ala Ile Gly Ile Leu Lys Leu Asn Lys Asp Glu
        495                 500                 505

aag aat cct aag gtg gca gag tta tac tca cca tta att tct gca cca   1588
Lys Asn Pro Lys Val Ala Glu Leu Tyr Ser Pro Leu Ile Ser Ala Pro
    510                 515                 520

atg gta agc gat gaa att gag cga cca aat gta gtt aaa tta ggt aat   1636
```

```
Met Val Ser Asp Glu Ile Glu Arg Pro Asn Val Val Lys Leu Gly Asn
525                 530                 535                 540

aaa tat tac tta ttt gcc gct acc cgt tta aat cga gga agt aat gat   1684
Lys Tyr Tyr Leu Phe Ala Ala Thr Arg Leu Asn Arg Gly Ser Asn Asp
                545                 550                 555

gat gct tgg atg aat gct aat tat gcc gtt ggt gat aat gtt gca atg   1732
Asp Ala Trp Met Asn Ala Asn Tyr Ala Val Gly Asp Asn Val Ala Met
            560                 565                 570

gtc gga tat gtt gct gat agt cta act gga tct tat aag cca tta aat   1780
Val Gly Tyr Val Ala Asp Ser Leu Thr Gly Ser Tyr Lys Pro Leu Asn
        575                 580                 585

gat tct gga gta gtc ttg act gct tct gtt cct gca aac tgg cgg aca   1828
Asp Ser Gly Val Val Leu Thr Ala Ser Val Pro Ala Asn Trp Arg Thr
    590                 595                 600

gca act tat tca tat tat gct gtc ccc gtt gcc gga aaa gat gac caa   1876
Ala Thr Tyr Ser Tyr Tyr Ala Val Pro Val Ala Gly Lys Asp Asp Gln
605                 610                 615                 620

gta tta gtt act tca tat atg act aat aga aat gga gta gcg ggt aaa   1924
Val Leu Val Thr Ser Tyr Met Thr Asn Arg Asn Gly Val Ala Gly Lys
                625                 630                 635

gga atg gat tca act tgg gca ccg agt ttc tta cta caa att aac ccg   1972
Gly Met Asp Ser Thr Trp Ala Pro Ser Phe Leu Leu Gln Ile Asn Pro
            640                 645                 650

gat aac aca act act gtt tta gct aaa atg act aat caa ggg gat tgg   2020
Asp Asn Thr Thr Thr Val Leu Ala Lys Met Thr Asn Gln Gly Asp Trp
        655                 660                 665

att tgg gat gat tca agc gaa aat ctt gat atg att ggt gat tta gac   2068
Ile Trp Asp Asp Ser Ser Glu Asn Leu Asp Met Ile Gly Asp Leu Asp
    670                 675                 680

tcc gct gct tta cct ggc gaa cgt gat aaa cct gtt gat tgg gac tta   2116
Ser Ala Ala Leu Pro Gly Glu Arg Asp Lys Pro Val Asp Trp Asp Leu
685                 690                 695                 700

att ggt tat gga tta aaa ccg cat gat cct gct aca cca aat gat cct   2164
Ile Gly Tyr Gly Leu Lys Pro His Asp Pro Ala Thr Pro Asn Asp Pro
                705                 710                 715

gaa acg cca act aca cca gaa acc cct gag aca cct aat act ccc aaa   2212
Glu Thr Pro Thr Thr Pro Glu Thr Pro Glu Thr Pro Asn Thr Pro Lys
            720                 725                 730

aca cca aag act cct gaa aat cct ggg aca cct caa act cct aat aca   2260
Thr Pro Lys Thr Pro Glu Asn Pro Gly Thr Pro Gln Thr Pro Asn Thr
        735                 740                 745

cct aat act ccg gaa att cct tta act cca gaa acg cct aag caa cct   2308
Pro Asn Thr Pro Glu Ile Pro Leu Thr Pro Glu Thr Pro Lys Gln Pro
    750                 755                 760

gaa acc caa act aat aat cgt ttg cca caa act gga aat aat gcc aat   2356
Glu Thr Gln Thr Asn Asn Arg Leu Pro Gln Thr Gly Asn Asn Ala Asn
```

```
765                 770                 775                 780

aaa gcc atg att ggc cta ggt atg gga aca ttg ctt agt atg ttt ggt   2404
Lys Ala Met Ile Gly Leu Gly Met Gly Thr Leu Leu Ser Met Phe Gly
                785                 790                 795

ctt gca gaa att aac aaa cgt cga ttt aac taaatacttt aaaataaaac     2454
Leu Ala Glu Ile Asn Lys Arg Arg Phe Asn
            800                 805

cgctaagcct taaattcagc ttaacggttt tttattttaa aagtttttat tgtaaaaaag 2514

cgaattatca ttaatactaa tgcaattgtt gtaagacctt acgacagtag taacaatgaa 2574

tttgcccatc tttgtcgg                                              2592
```

<210> 5
<211> 5
<212> PRT
<213> Lactobacillus reuteri

<220>
<221> MOD_RES
<222> (3)
<223> Any amino acid

<400> 5
Leu Pro Xaa Thr Gly
1   5

<210> 6
<211> 27
<212> PRT
<213> Lactobacillus reuteri

<400> 6
Ala Gln Val Glu Ser Asn Asn Tyr Asn Gly Val Ala Glu Val Asn Thr
1   5   10   15

Glu Arg Gln Ala Asn Gly Gln Ile Gly Val Asp
            20   25

<210> 7
<211> 16
<212> PRT
<213> Lactobacillus reuteri

<400> 7
Met Ala His Leu Asp Val Trp Asp Ser Trp Pro Val Gln Asp Pro Val
1   5   10   15

<210> 8
<211> 9
<212> PRT
<213> Lactobacillus reuteri

<400> 8

Asn Ala Gly Ser Ile Phe Gly Thr Lys
1 5

<210> 9
<211> 19
<212> PRT
<213> Lactobacillus reuteri

<400> 9
Val Glu Glu Val Tyr Ser Pro Lys Val Ser Thr Leu Met Ala Ser Asp
1 5 10 15

Glu Val Glu

<210> 10
<211> 4634
<212> DNA
<213> Lactobacillus reuteri

<220>
<221> CDS
<222> (1220)..(3598)

<220>
<221> RBS
<222> (1205)..(1210)

<220>
<221> modified_base
<222> (2702)..(2707)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (3686)..(3698)
<223> a, c, t, g, other or unknown

<400> 10
gttaacaaag acaaaatttt atataattct tcaaattaaa tttcccactg taagaacata 60

aatgggtacc tgtttgatgg gaataatata tttgtaacta accggccggc acctctttct 120

aatgtgccta ggatgcataa tggatgtaaa ttactagatg gcggttttta tacattaacc 180

tcgcaggaga gaaaagaagc aattagtaag gatccatatg cagataaatt tattaggcct 240

tatttaggtg ctaaaaattt cattcatgga actgctaggt actgtatttg gttaaaggac 300

gcaaacccga aagatatcca tcaatcgcca tttatactgg atagaatcaa taaagtagcg 360

gaattcagat cgcagcaaaa aagtaaagat acacaaaaat atgcaaaacg gcccatgcta 420

acaacacgac ttgcctatta tagccacgat gtacatacgg atatgctgat agtacctgca 480

acatcatcgc aacgtagaga atatcttcca attggatatg tttcagaaaa gaatattgtg 540

tcttattcac taatgctaat ccccaatgct agtaatttta atttcggtat tctagaatct 600

aaagttcact atatttggtt aaaaaacttt tgcggtcggt tgaagtccga ttatcgttat 660

```
tcaaacacta ttatttataa taatttccct tggccgactg ttggtgacaa gccaggamca 720

acaccatctc tgacactcgc tcaaggtata ttaaatactc gcaagctcta tccagacagc 780

tcactggctg atctttatga tccactaaca atgccragtt gaactcgtaa agctcatgaa 840

gccaatgata aagctgttct taaagcatat ggattgagcc ctaaagctac tgagcaagaa 900

atcgtagaac atctatttaa gatgtatgaa aaactgacta aaggtgaaag ataactttgt 960

aaaaccaata ttttataaag acagtaaatg ttaatttgat aaaaacatat atttaataaa 1020

caaaagtgat ataatcaagt agttctttgt attacaaaat acatttaata tctctcagca 1080

ttttgcatac tgggagattt tttattgaca aattgtttga aagtgcttat gatgaaaccg 1140

tgtagaaact aattcaattt gataaacgtt agacatttct gaggaggaag tcattttgga 1200

gtacaaagaa cataagaaa atg tat aaa gtc ggc aag aat tgg gcc gtt gct  1252
                    Met Tyr Lys Val Gly Lys Asn Trp Ala Val Ala
                      1               5                  10

aca ttg gta tca gct tca att tta atg gga ggg gtt gta acc gct cat   1300
Thr Leu Val Ser Ala Ser Ile Leu Met Gly Gly Val Val Thr Ala His
          15                  20                  25

gct gat caa gta gaa agt aac aat tac aac ggt gtt gct gaa gtt aat   1348
Ala Asp Gln Val Glu Ser Asn Asn Tyr Asn Gly Val Ala Glu Val Asn
        30                  35                  40

act gaa cgt caa gct aat ggt caa att ggc gta gat gga aaa att att   1396
Thr Glu Arg Gln Ala Asn Gly Gln Ile Gly Val Asp Gly Lys Ile Ile
     45                  50                  55

agt gct aac agt aat aca acc agt ggc tcg aca aat caa gaa tca tct   1444
Ser Ala Asn Ser Asn Thr Thr Ser Gly Ser Thr Asn Gln Glu Ser Ser
 60                  65                  70                  75

gct act aac aat act gaa aat gct gtt gtt aat gaa agc aaa aat act   1492
Ala Thr Asn Asn Thr Glu Asn Ala Val Val Asn Glu Ser Lys Asn Thr
                80                  85                  90

aac aat act gaa aat gct gtt gtt aat gaa aac aaa aat act aac aat   1540
Asn Asn Thr Glu Asn Ala Val Val Asn Glu Asn Lys Asn Thr Asn Asn
            95                  100                 105

act gaa aat gct gtt gtt aat gaa aac aaa aat act aac aac aca gaa   1588
Thr Glu Asn Ala Val Val Asn Glu Asn Lys Asn Thr Asn Asn Thr Glu
        110                 115                 120

aac gat aat agt caa tta aag tta act aat aat gaa caa cca tca gcc   1636
Asn Asp Asn Ser Gln Leu Lys Leu Thr Asn Asn Glu Gln Pro Ser Ala
    125                 130                 135

gct act caa gca aac ttg aag aag cta aat cct caa gct gct aag gct   1684
Ala Thr Gln Ala Asn Leu Lys Lys Leu Asn Pro Gln Ala Ala Lys Ala
140                 145                 150                 155

gtt caa aat gcc aag att gat gcc ggt agt tta aca gat gat caa att   1732
Val Gln Asn Ala Lys Ile Asp Ala Gly Ser Leu Thr Asp Asp Gln Ile
```

```
                160                 165                 170

aat gaa tta aat aag att aac ttc tct aag tct gct gaa aag ggt gca   1780
Asn Glu Leu Asn Lys Ile Asn Phe Ser Lys Ser Ala Glu Lys Gly Ala
            175                 180                 185

aaa ttg acc ttt aag gac tta gag ggg att ggt aat gct att gtt aag   1828
Lys Leu Thr Phe Lys Asp Leu Glu Gly Ile Gly Asn Ala Ile Val Lys
        190                 195                 200

caa gat cca caa tat gct att cct tat tct aat gct aag gaa atc aag   1876
Gln Asp Pro Gln Tyr Ala Ile Pro Tyr Ser Asn Ala Lys Glu Ile Lys
    205                 210                 215

aat atg cct gca aca tac act gta gat gcc caa aca ggt aag atg gct   1924
Asn Met Pro Ala Thr Tyr Thr Val Asp Ala Gln Thr Gly Lys Met Ala
220                 225                 230                 235

cat ctt gat gtc tgg gac tct tgg cca gta caa gat cct gtc aca ggt   1972
His Leu Asp Val Trp Asp Ser Trp Pro Val Gln Asp Pro Val Thr Gly
                240                 245                 250

tat gta tct aat tac atg ggt tat caa cta gtt att gct atg atg ggt   2020
Tyr Val Ser Asn Tyr Met Gly Tyr Gln Leu Val Ile Ala Met Met Gly
            255                 260                 265

att cca aat tcg cca act gga gat aat cat atc tat ctt ctt tac aac   2068
Ile Pro Asn Ser Pro Thr Gly Asp Asn His Ile Tyr Leu Leu Tyr Asn
        270                 275                 280

aag tat ggt gat aat gac ttt tct cat tgg cgc aat gca ggt tca atc   2116
Lys Tyr Gly Asp Asn Asp Phe Ser His Trp Arg Asn Ala Gly Ser Ile
    285                 290                 295

ttt gga act aaa gaa aca aat gtg ttc caa gaa tgg tca ggt tca gct   2164
Phe Gly Thr Lys Glu Thr Asn Val Phe Gln Glu Trp Ser Gly Ser Ala
300                 305                 310                 315

att gta aat gat gat ggt aca att caa cta ttt ttc acc tca aat gat   2212
Ile Val Asn Asp Asp Gly Thr Ile Gln Leu Phe Phe Thr Ser Asn Asp
                320                 325                 330

acg tct gat tac aag ttg aat gat caa cgc ctt gct acc gca aca tta   2260
Thr Ser Asp Tyr Lys Leu Asn Asp Gln Arg Leu Ala Thr Ala Thr Leu
            335                 340                 345

aac ctt aat gtt gat gat aac ggt gtt tca atc aag agt gtt gat aat   2308
Asn Leu Asn Val Asp Asp Asn Gly Val Ser Ile Lys Ser Val Asp Asn
        350                 355                 360

tat caa gtt ttg ttt gaa ggt gat gga ttt cac tac caa act tat gaa   2356
Tyr Gln Val Leu Phe Glu Gly Asp Gly Phe His Tyr Gln Thr Tyr Glu
    365                 370                 375

caa ttc gca aac ggc aaa gat cgt gaa aat gat gat tac tgc tta cgt   2404
Gln Phe Ala Asn Gly Lys Asp Arg Glu Asn Asp Asp Tyr Cys Leu Arg
380                 385                 390                 395

gac cca cac gtt gtt caa tta gaa aat ggt gat cgt tat ctt gta ttc   2452
Asp Pro His Val Val Gln Leu Glu Asn Gly Asp Arg Tyr Leu Val Phe
                400                 405                 410
```

```
gaa gct aat act ggg aca gaa gat tac caa agt gac gac caa att tat   2500
Glu Ala Asn Thr Gly Thr Glu Asp Tyr Gln Ser Asp Asp Gln Ile Tyr
            415                 420                 425

aat tgg gct aac tat ggt ggc gat gat gcc ttc aat att aag agt tcc   2548
Asn Trp Ala Asn Tyr Gly Gly Asp Asp Ala Phe Asn Ile Lys Ser Ser
        430                 435                 440

ttc aag ctt ttg aat aat aag aag gat cgt gaa ttg gct ggt tta gct   2596
Phe Lys Leu Leu Asn Asn Lys Lys Asp Arg Glu Leu Ala Gly Leu Ala
    445                 450                 455

aat ggt gca ctt ggt atc tta aag ctc act aac aat caa agt aag cca   2644
Asn Gly Ala Leu Gly Ile Leu Lys Leu Thr Asn Asn Gln Ser Lys Pro
460                 465                 470                 475

aag gtt gaa gaa gta tac tca cca ttg gta tct act ttg atg gct tgc   2692
Lys Val Glu Glu Val Tyr Ser Pro Leu Val Ser Thr Leu Met Ala Cys
                480                 485                 490

gat gag gta nnn nnn aag ctt ggt gat aag tat tat ctc ttc tcc gta   2740
Asp Glu Val Xaa Xaa Lys Leu Gly Asp Lys Tyr Tyr Leu Phe Ser Val
            495                 500                 505

act cgt gta agt cgt ggt tcc gat cgt gaa tta acc gct aag gat aac   2788
Thr Arg Val Ser Arg Gly Ser Asp Arg Glu Leu Thr Ala Lys Asp Asn
        510                 515                 520

aca atc gtt ggt gat aac gtt gct atg att ggt tac gtt tcc gat agc   2836
Thr Ile Val Gly Asp Asn Val Ala Met Ile Gly Tyr Val Ser Asp Ser
    525                 530                 535

tta atg ggt aag tac aag cca tta aat aac tca ggt gtc gta tta act   2884
Leu Met Gly Lys Tyr Lys Pro Leu Asn Asn Ser Gly Val Val Leu Thr
540                 545                 550                 555

gca tca gta cct gca aac tgg cgt act gct act tat tcc tac tat gca   2932
Ala Ser Val Pro Ala Asn Trp Arg Thr Ala Thr Tyr Ser Tyr Tyr Ala
                560                 565                 570

gta cct gta gct ggt cat cct gat caa gta tta att act tct tac atg   2980
Val Pro Val Ala Gly His Pro Asp Gln Val Leu Ile Thr Ser Tyr Met
            575                 580                 585

agt aac aag gac ttt gct tca ggt gaa gga aac tat gca act tgg gca   3028
Ser Asn Lys Asp Phe Ala Ser Gly Glu Gly Asn Tyr Ala Thr Trp Ala
        590                 595                 600

cca agt ttc tta gta caa atc aat cca gat gac acg aca act gta tta   3076
Pro Ser Phe Leu Val Gln Ile Asn Pro Asp Asp Thr Thr Thr Val Leu
    605                 610                 615

gca cgt gca act aac caa ggt gac tgg gtg tgg gac gac tct agt cgg   3124
Ala Arg Ala Thr Asn Gln Gly Asp Trp Val Trp Asp Asp Ser Ser Arg
620                 625                 630                 635

aac gat aat atg ctc ggt gtt ctt aaa gaa ggt gca gct aac agt gcc   3172
Asn Asp Asn Met Leu Gly Val Leu Lys Glu Gly Ala Ala Asn Ser Ala
                640                 645                 650
```

```
gcc tta cca ggt gaa tgg ggt aag cca gtt gac tgg agt ttg att aac   3220
Ala Leu Pro Gly Glu Trp Gly Lys Pro Val Asp Trp Ser Leu Ile Asn
            655                 660                 665

aga agt cct ggc tta ggc tta aag cct cat caa cca gtt caa cca aag   3268
Arg Ser Pro Gly Leu Gly Leu Lys Pro His Gln Pro Val Gln Pro Lys
        670                 675                 680

att gat caa cct gat caa caa cct tct ggt caa aac act aag aat gtc   3316
Ile Asp Gln Pro Asp Gln Gln Pro Ser Gly Gln Asn Thr Lys Asn Val
    685                 690                 695

aca cca ggt aat ggt gat aag cct gct ggt aag gca act cct gat aac   3364
Thr Pro Gly Asn Gly Asp Lys Pro Ala Gly Lys Ala Thr Pro Asp Asn
700                 705                 710                 715

act aat att gat cca agt gca caa cct tct ggt caa aac act aat att   3412
Thr Asn Ile Asp Pro Ser Ala Gln Pro Ser Gly Gln Asn Thr Asn Ile
                720                 725                 730

gat cca agt gca caa mct tct ggt caa aac act aag aat gtc aca cca   3460
Asp Pro Ser Ala Gln Xaa Ser Gly Gln Asn Thr Lys Asn Val Thr Pro
            735                 740                 745

ggt aat gag aaa caa ggt aag aat acc gat gca aaa caa tta cca caa   3508
Gly Asn Glu Lys Gln Gly Lys Asn Thr Asp Ala Lys Gln Leu Pro Gln
        750                 755                 760

aca ggt aat aag tct ggt tta gca gga ctt tac gct ggt tca tta ctt   3556
Thr Gly Asn Lys Ser Gly Leu Ala Gly Leu Tyr Ala Gly Ser Leu Leu
    765                 770                 775

gcc ttg ttt gga ttg gca gca att gaa aag cgt cac gct taa           3598
Ala Leu Phe Gly Leu Ala Ala Ile Glu Lys Arg His Ala
780                 785                 790

tagagtaaaa aaacatcctc cactcaagtt acaagtagga taatatgtat tatttctacg 3658

cytagtcaag aggrattact ggacatannn nnnnnnnnnn tccagttacc aagtggaata 3718

tagtattatt ccacgctagt caggaggatt actgacatta ttggctacat ggccggtagt 3778

cctcttttct tttgtgacga attgtcaaac caagtgcaac ggtttctcaa aaaacacctc 3838

atatggggtt tcataattta acacttttcg aggacggcgg ttcagctgat gttggcagaa 3898

actgacgtcc ttatctgtat aatcatcaat attagccctt ttaggaaagt attccctaat 3958

tagsccattg gtattttcat tgggtcctct ttcctctggt gaatagggat ctggccaata 4018

gatagctact cctaaacgtc ctcgaatatc attcaagcca agaaattcac gcccatgatc 4078

tggagtcaat gaatggacaa attctttagg aatagaccct aagagatcaa ttaagccctg 4138

atatttgaat tcggagaagg ggagttgtcc aacaattgcc gttataatac cagggttaat 4198

acggccctgg gcctctacgg taatattgta tttttggctc agatcagtga tagaaaccca 4258

cagatttagc ttgccggtgg agtgctgctt gaagtcttca attacttcgt taccatgttt 4318

gattgctaat ctgatgtgtc gttgttgtgg tgtagtaggc atcataccac ctcctcataa 4378
```

aataaggtat aacaggaatt tcttgtacta tatgatcctt ccaatataat aatattaggc 4438

cgataagaaa tgaccagcta ccatttcttg atgcttagtg aatataatcg gatgatacgt 4498

caccctcaa caatccaatt tcacggaggt gagtaatcat gccgagagct aggaatgatt 4558

ggaggaacga acacggtcca tgcggcagtg gctatttgga ttttagccaa agcagcgtta 4618

ctgcttgcaa aagctt 4634

<210> 11
<211> 792
<212> PRT
<213> Lactobacillus reuteri

<220>
<221> MOD_RES
<222> (495)..(496)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (737)
<223> Thr or Pro

<400> 11

```
Met Tyr Lys Val Gly Lys Asn Trp Ala Val Ala Thr Leu Val Ser Ala
  1               5                  10                  15

Ser Ile Leu Met Gly Gly Val Val Thr Ala His Ala Asp Gln Val Glu
             20                  25                  30

Ser Asn Asn Tyr Asn Gly Val Ala Glu Val Asn Thr Glu Arg Gln Ala
         35                  40                  45

Asn Gly Gln Ile Gly Val Asp Gly Lys Ile Ile Ser Ala Asn Ser Asn
     50                  55                  60

Thr Thr Ser Gly Ser Thr Asn Gln Glu Ser Ser Ala Thr Asn Asn Thr
 65                  70                  75                  80

Glu Asn Ala Val Val Asn Glu Ser Lys Asn Thr Asn Asn Thr Glu Asn
                 85                  90                  95

Ala Val Val Asn Glu Asn Lys Asn Thr Asn Asn Thr Glu Asn Ala Val
            100                 105                 110

Val Asn Glu Asn Lys Asn Thr Asn Asn Thr Glu Asn Asp Asn Ser Gln
        115                 120                 125

Leu Lys Leu Thr Asn Asn Glu Gln Pro Ser Ala Ala Thr Gln Ala Asn
    130                 135                 140

Leu Lys Lys Leu Asn Pro Gln Ala Ala Lys Ala Val Gln Asn Ala Lys
145                 150                 155                 160

Ile Asp Ala Gly Ser Leu Thr Asp Asp Gln Ile Asn Glu Leu Asn Lys
                165                 170                 175
```

```
Ile Asn Phe Ser Lys Ser Ala Glu Lys Gly Ala Lys Leu Thr Phe Lys
            180                 185                 190

Asp Leu Glu Gly Ile Gly Asn Ala Ile Val Lys Gln Asp Pro Gln Tyr
        195                 200                 205

Ala Ile Pro Tyr Ser Asn Ala Lys Glu Ile Lys Asn Met Pro Ala Thr
    210                 215                 220

Tyr Thr Val Asp Ala Gln Thr Gly Lys Met Ala His Leu Asp Val Trp
225                 230                 235                 240

Asp Ser Trp Pro Val Gln Asp Pro Val Thr Gly Tyr Val Ser Asn Tyr
                245                 250                 255

Met Gly Tyr Gln Leu Val Ile Ala Met Met Gly Ile Pro Asn Ser Pro
            260                 265                 270

Thr Gly Asp Asn His Ile Tyr Leu Leu Tyr Asn Lys Tyr Gly Asp Asn
        275                 280                 285

Asp Phe Ser His Trp Arg Asn Ala Gly Ser Ile Phe Gly Thr Lys Glu
    290                 295                 300

Thr Asn Val Phe Gln Glu Trp Ser Gly Ser Ala Ile Val Asn Asp Asp
305                 310                 315                 320

Gly Thr Ile Gln Leu Phe Phe Thr Ser Asn Asp Thr Ser Asp Tyr Lys
                325                 330                 335

Leu Asn Asp Gln Arg Leu Ala Thr Ala Thr Leu Asn Leu Asn Val Asp
            340                 345                 350

Asp Asn Gly Val Ser Ile Lys Ser Val Asp Asn Tyr Gln Val Leu Phe
        355                 360                 365

Glu Gly Asp Gly Phe His Tyr Gln Thr Tyr Glu Gln Phe Ala Asn Gly
    370                 375                 380

Lys Asp Arg Glu Asn Asp Asp Tyr Cys Leu Arg Asp Pro His Val Val
385                 390                 395                 400

Gln Leu Glu Asn Gly Asp Arg Tyr Leu Val Phe Glu Ala Asn Thr Gly
                405                 410                 415

Thr Glu Asp Tyr Gln Ser Asp Asp Gln Ile Tyr Asn Trp Ala Asn Tyr
            420                 425                 430

Gly Gly Asp Asp Ala Phe Asn Ile Lys Ser Ser Phe Lys Leu Leu Asn
        435                 440                 445

Asn Lys Lys Asp Arg Glu Leu Ala Gly Leu Ala Asn Gly Ala Leu Gly
    450                 455                 460

Ile Leu Lys Leu Thr Asn Asn Gln Ser Lys Pro Lys Val Glu Glu Val
465                 470                 475                 480

Tyr Ser Pro Leu Val Ser Thr Leu Met Ala Cys Asp Glu Val Xaa Xaa
                485                 490                 495

Lys Leu Gly Asp Lys Tyr Tyr Leu Phe Ser Val Thr Arg Val Ser Arg
```

```
            500                 505                 510

Gly Ser Asp Arg Glu Leu Thr Ala Lys Asp Asn Thr Ile Val Gly Asp
        515                 520                 525

Asn Val Ala Met Ile Gly Tyr Val Ser Asp Ser Leu Met Gly Lys Tyr
    530                 535                 540

Lys Pro Leu Asn Asn Ser Gly Val Val Leu Thr Ala Ser Val Pro Ala
545                 550                 555                 560

Asn Trp Arg Thr Ala Thr Tyr Ser Tyr Tyr Ala Val Pro Val Ala Gly
                565                 570                 575

His Pro Asp Gln Val Leu Ile Thr Ser Tyr Met Ser Asn Lys Asp Phe
            580                 585                 590

Ala Ser Gly Glu Gly Asn Tyr Ala Thr Trp Ala Pro Ser Phe Leu Val
        595                 600                 605

Gln Ile Asn Pro Asp Asp Thr Thr Thr Val Leu Ala Arg Ala Thr Asn
    610                 615                 620

Gln Gly Asp Trp Val Trp Asp Asp Ser Ser Arg Asn Asp Asn Met Leu
625                 630                 635                 640

Gly Val Leu Lys Glu Gly Ala Ala Asn Ser Ala Ala Leu Pro Gly Glu
                645                 650                 655

Trp Gly Lys Pro Val Asp Trp Ser Leu Ile Asn Arg Ser Pro Gly Leu
            660                 665                 670

Gly Leu Lys Pro His Gln Pro Val Gln Pro Lys Ile Asp Gln Pro Asp
        675                 680                 685

Gln Gln Pro Ser Gly Gln Asn Thr Lys Asn Val Thr Pro Gly Asn Gly
    690                 695                 700

Asp Lys Pro Ala Gly Lys Ala Thr Pro Asp Asn Thr Asn Ile Asp Pro
705                 710                 715                 720

Ser Ala Gln Pro Ser Gly Gln Asn Thr Asn Ile Asp Pro Ser Ala Gln
                725                 730                 735

Xaa Ser Gly Gln Asn Thr Lys Asn Val Thr Pro Gly Asn Glu Lys Gln
            740                 745                 750

Gly Lys Asn Thr Asp Ala Lys Gln Leu Pro Gln Thr Gly Asn Lys Ser
        755                 760                 765

Gly Leu Ala Gly Leu Tyr Ala Gly Ser Leu Leu Ala Leu Phe Gly Leu
    770                 775                 780

Ala Ala Ile Glu Lys Arg His Ala
785                 790
```

<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
ctgataataa tggaaatgta tcac 24

<210> 13
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 13
catgatcata agtttggtag taatag 26

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 14
gtgatacatt tccattatta tcag 24

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
ctattactac caaacttatg atcatg 26

<210> 16
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
ccatggccat ggtagaacgc aaggaacata aaaaaatg 38

<210> 17
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
agatctagat ctgttaaatc gacgtttgtt aatttctg 38

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> modified_base
<222> (6)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (15)
<223> a, c, t, g, other or unknown

<400> 18
gaygtntggg aywsntgggc c 21

<210> 19
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (3)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (6)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (9)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (12)
<223> a, c, t, g, other or unknown

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
gtngcnswnc cnswccayts ytg 23

<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
gaatgtaggt ccaatttttg gc 22

<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
cctgtccgaa catcttgaac tg 22

<210> 22
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> modified_base
<222> (6)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (9)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (12)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (18)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (21)
<223> a, c, t, g, other or unknown

<400> 22
arraanswng gngcvmangt nsw 23

<210> 23
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> modified_base
<222> (9)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (11)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (15)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (21)
<223> a, c, t, g, other or unknown

<400> 23
tayaayggng tngcngargt naa 23

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
ccgaccatct tgtttgatta ac 22

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
aaytataayg gygttgcryg aagt 24

<210> 26
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> modified_base
<222> (9)
<223> a, c, t, g, other or unknown

<400> 26
taccgnwsnc tacttcaact t 21

<210> 27
<211> 17
<212> PRT
<213> Lactobacillus reuteri

<400> 27
Tyr Asn Gly Val Ala Glu Val Lys Lys Arg Gly Tyr Phe Tyr Ala Arg
1 5 10 15

Thr

<210> 28
<211> 17
<212> PRT
<213> Lactobacillus reuteri

<400> 28
Tyr Asn Gly Val Ala Glu Val Asn Thr Glu Arg Gln Ala Asn Gly Gly
1 5 10 15

Ile

<210> 29
<211> 14
<212> PRT
<213> Bacillus amyloliquefaciens

<400> 29
Gly Leu Asp Val Trp Asp Ser Trp Pro Leu Gln Asn Ala Asp
1 5 10

<210> 30
<211> 14
<212> PRT
<213> Bacillus subtilis

<400> 30
Gly Leu Asp Val Trp Asp Ser Trp Pro Leu Gln Asn Ala Asp
1 5 10

<210> 31
<211> 14
<212> PRT
<213> Streptococcus mutans

<400> 31
Asp Leu Asp Val Trp Asp Ser Trp Pro Val Gln Asp Ala Lys
1 5 10

<210> 32
<211> 14
<212> PRT
<213> Streptococcus salivarius

<400> 32
Glu Ile Asp Val Trp Asp Ser Trp Pro Val Gln Asp Ala Lys
1 5 10

<210> 33
<211> 16
<212> PRT
<213> Bacillus amyloliquefaciens

<400> 33
Gln Thr Gln Glu Trp Ser Gly Ser Ala Thr Phe Thr Ser Asp Gly Lys
1 5 10 15

<210> 34
<211> 16
<212> PRT
<213> Bacillus subtilis

<400> 34
Gln Thr Gln Glu Trp Ser Gly Ser Ala Thr Phe Thr Ser Asp Gly Lys
1 5 10 15

<210> 35
<211> 16
<212> PRT
<213> Streptococcus mutans

<400> 35
Leu Thr Gln Glu Trp Ser Gly Ser Ala Thr Val Asn Glu Asp Gly Ser
1 5 10 15

<210> 36
<211> 16
<212> PRT
<213> Streptococcus salivarius

<400> 36
Asp Asp Gln Gln Trp Ser Gly Ser Ala Thr Val Asn Ser Asp Gly Ser
1 5 10 15

<210> 37
<211> 11
<212> PRT
<213> Bacillus amyloliquefaciens

<400> 37

Lys Ala Thr Phe Gly Pro Ser Phe Leu Met Asn
1 5 10

<210> 38
<211> 11
<212> PRT
<213> Bacillus subtilis

<400> 38
Gln Ser Thr Phe Ala Pro Ser Phe Leu Leu Asn
1 5 10

<210> 39
<211> 11
<212> PRT
<213> Streptococcus mutans

<400> 39
Asn Ser Thr Trp Ala Pro Ser Phe Leu Ile Gln
1 5 10

<210> 40
<211> 11
<212> PRT
<213> Streptococcus salivarius

<400> 40
Lys Ser Thr Trp Ala Pro Ser Phe Leu Ile Lys
1 5 10